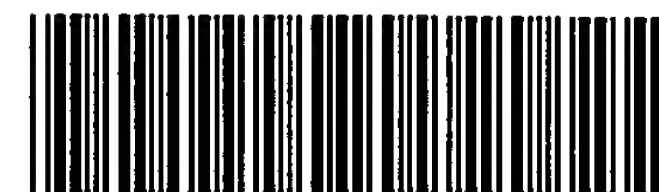


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/845, 157 B
Source: IFW0
Date Processed by STIC: 08/01/2005

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IFW16

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DATE: 08/01/2005

PATENT APPLICATION: US/09/845,157B

TIME: 16:16:15

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5 <110> APPLICANT: Smith, Michael D.
6      Potter, Robert J.
7      Dhariwal, Gulshan
8      Gerard, Gary F.
9      Rosenthal, Kim
11 <120> TITLE OF INVENTION: Thermostable Reverse Transcriptases and Uses Thereof
13 <130> FILE REFERENCE: 0942.5040001/RWE/AWL
15 <140> CURRENT APPLICATION NUMBER: US 09/845,157B
16 <141> CURRENT FILING DATE: 2001-05-01
18 <150> PRIOR APPLICATION NUMBER: US 60/207,196
19 <151> PRIOR FILING DATE: 2000-05-26
22 <160> NUMBER OF SEQ ID NOS: 8
24 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2151
29 <212> TYPE: DNA
30 <213> ORGANISM: Moloney-Murine Leukemia Virus
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34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(2151)
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43 ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag cat      96
44 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys His
45          20          25          30
47 atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa      144
48 Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
49          35          40          45
51 gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag      192
52 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
53          50          55          60
55 gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct      240
56 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
57 65          70          75          80
59 ctg atc ata ctt ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa      288
60 Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
61          85          90          95
63 tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag      336
64 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
65          100          105          110
67 aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac      384

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69			115					120					125				
71	acg	ccc	ctg	cta	ccc	gtc	aag	aaa	ccc	ggg	act	aat	gat	tac	agg	cct	432
72	Thr	Pro	Leu	Leu	Pro	Val	Lys	Lys	Pro	Gly	Thr	Asn	Asp	Tyr	Arg	Pro	
73			130					135					140				
75	gtc	caa	gat	ctg	aga	gag	gtc	aac	aaa	cgc	gta	gaa	gac	atc	cac	ccc	480
76	Val	Gln	Asp	Leu	Arg	Glu	Val	Asn	Lys	Arg	Val	Glu	Asp	Ile	His	Pro	
77	145						150					155				160	
79	acc	gta	ccc	aac	ccc	tac	aac	ctc	ttg	agt	ggg	ctc	cca	ccg	tcc	cac	528
80	Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Pro	Pro	Ser	His	
81					165					170					175		
83	cag	tgg	tac	act	ggt	cta	gac	tta	aaa	gat	gcc	ttt	ttc	tgc	ctg	aga	576
84	Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe	Phe	Cys	Leu	Arg	
85				180					185					190			
87	ctc	cac	ccg	acg	tct	cag	cct	ctc	ttc	gcc	ttt	gaa	tgg	aga	gac	cca	624
88	Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu	Trp	Arg	Asp	Pro	
89			195					200					205				
91	gag	atg	gga	atc	tct	ggc	caa	cta	acc	tgg	acc	aga	ctc	cca	cag	gga	672
92	Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg	Leu	Pro	Gln	Gly	
93		210					215					220					
95	ttc	aaa	aac	agt	ccc	acc	ctg	ttt	gat	gag	gca	ctg	cgc	aga	gac	cta	720
96	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	Arg	Arg	Asp	Leu	
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101					245					250				255			
103	gat	gac	tta	ctg	ctg	gcc	gcc	act	tct	gag	ctc	gac	tgc	caa	caa	ggt	816
104	Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp	Cys	Gln	Gln	Gly	
105				260						265				270			
107	act	cgg	gcc	ctg	tta	caa	acc	cta	gga	gac	ctc	ggg	tat	cgg	gcc	tcg	864
108	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asp	Leu	Gly	Tyr	Arg	Ala	Ser	
109				275				280					285				
111	gcc	aag	aaa	gcc	caa	att	tgc	cag	aaa	cag	gtc	aag	tat	ctg	ggg	tat	912
112	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys	Tyr	Leu	Gly	Tyr	
113		290					295					300					
115	ctt	cta	aaa	gag	ggt	cag	aga	tgg	ctg	act	gag	gcc	aga	aaa	gag	act	960
116	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala	Arg	Lys	Glu	Thr	
117	305					310					315				320		
119	gtg	atg	ggg	cag	cct	act	ccg	aag	acc	ccg	cgg	caa	cta	agg	gag	ttc	1008
120	Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	Leu	Arg	Glu	Phe	
121					325					330				335			
123	cta	ggg	acg	gca	ggc	ttc	tgt	cgc	ctc	tgg	atc	cct	ggg	ttt	gca	gaa	1056
124	Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro	Gly	Phe	Ala	Glu	
125				340					345				350				
127	atg	gca	gcc	ccc	ttg	tac	cct	ctc	acc	aaa	acg	ggg	act	ctg	ttt	aat	1104
128	Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly	Thr	Leu	Phe	Asn	
129			355					360				365					
131	tgg	ggc	cca	gac	caa	caa	aag	gcc	tat	caa	gaa	atc	aag	caa	gct	ctt	1152
132	Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile	Lys	Gln	Ala	Leu	

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139	ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa	1248		
140	Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln			
141		405	410	415
143	aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg tcc aaa aag cta	1296		
144	Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu			
145		420	425	430
147	gac cca gta gca gct ggg tgg ccc cct tgc cta cgg atg gta gca gcc	1344		
148	Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala			
149		435	440	445
151	att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca	1392		
152	Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro			
153		450	455	460
155	cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc	1440		
156	Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro			
157	465	470	475	480
159	ccc gat cga tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg	1488		
160	Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu			
161		485	490	495
163	ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac	1536		
164	Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn			
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167	ccg gct aca ctg ctc cca ctg cct gag gaa ggg ctg cag cac aac tgc	1584		
168	Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys			
169		515	520	525
171	ctt gat atc ctg gcc gaa gcc cac gga acc cga ccc gac cta acg gac	1632		
172	Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp			
173		530	535	540
175	cag ccg ctc cca gac gcc gac cac acc tgg tac acg ggt gga tcc agt	1680		
176	Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser			
177	545	550	555	560
179	ctc ttg caa gag gga cag cgt aag gcg gga gct gcg gtg acc acc gag	1728		
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183	acc gag gta atc tgg gct aaa gcc ctg cca gcc ggg aca tcc gct cag	1776		
184	Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln			
185		580	585	590
187	cgg gct cag ctg ata gca ctc acc cag gcc cta agg atg gca gaa ggt	1824		
188	Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly			
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191	aag aag cta aat gtt tat acg aat tcc cgt tat gct ttt gct act gcc	1872		
192	Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala			
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197	625	630	635	640

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203 ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa      2016
204 Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln
205          660          665          670
207 aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg      2064
208 Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
209          675          680          685
211 gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc      2112
212 Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu
213          690          695          700
215 ata gaa aat tca tca ccc aat tcc cgc tta att aat taa      2151
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217 705          710          715
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222 <212> TYPE: PRT
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235 Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
236          35          40          45
238 Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
239          50          55          60
241 Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
242 65          70          75          80
244 Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
245          85          90          95
247 Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
248          100         105         110
250 Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
251          115         120         125
253 Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
254          130         135         140
256 Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
257 145         150         155         160
259 Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
260          165         170         175
262 Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
263          180         185         190
265 Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
266          195         200         205
268 Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
269          210         215         220
271 Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu

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278				260					265					270		
280	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asp	Leu	Gly	Tyr	Arg	Ala	Ser
281			275					280					285			
283	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys	Tyr	Leu	Gly	Tyr
284		290					295				300					
285	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala	Arg	Lys	Glu	Thr
286	305					310				315					320	
288	Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	Leu	Arg	Glu	Phe
289				325						330					335	
291	Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro	Gly	Phe	Ala	Glu
292				340					345					350		
294	Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly	Thr	Leu	Phe	Asn
295			355					360					365			
297	Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile	Lys	Gln	Ala	Leu
298		370					375				380					
300	Leu	Thr	Ala	Pro	Ala	Leu	Gly	Leu	Pro	Asp	Leu	Thr	Lys	Pro	Phe	Glu
301	385					390				395						400
303	Leu	Phe	Val	Asp	Glu	Lys	Gln	Gly	Tyr	Ala	Lys	Gly	Val	Leu	Thr	Gln
304				405						410					415	
306	Lys	Leu	Gly	Pro	Trp	Arg	Arg	Pro	Val	Ala	Tyr	Leu	Ser	Lys	Lys	Leu
307				420					425					430		
309	Asp	Pro	Val	Ala	Ala	Gly	Trp	Pro	Pro	Cys	Leu	Arg	Met	Val	Ala	Ala
310			435					440					445			
312	Ile	Ala	Val	Leu	Thr	Lys	Asp	Ala	Gly	Lys	Leu	Thr	Met	Gly	Gln	Pro
313		450					455					460				
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316	465					470				475					480	
318	Pro	Asp	Arg	Trp	Leu	Ser	Asn	Ala	Arg	Met	Thr	His	Tyr	Gln	Ala	Leu
319				485					490						495	
321	Leu	Leu	Asp	Thr	Asp	Arg	Val	Gln	Phe	Gly	Pro	Val	Val	Ala	Leu	Asn
322				500					505					510		
324	Pro	Ala	Thr	Leu	Leu	Pro	Leu	Pro	Glu	Glu	Gly	Leu	Gln	His	Asn	Cys
325			515					520					525			
327	Leu	Asp	Ile	Leu	Ala	Glu	Ala	His	Gly	Thr	Arg	Pro	Asp	Leu	Thr	Asp
328		530					535					540				
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331	545					550				555					560	
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334				565					570						575	
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5

VERIFICATION SUMMARY

DATE: 08/01/2005

PATENT APPLICATION: US/09/845,157B

TIME: 16:16:16

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